PATENT

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U.G.J
4/13/00

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants:	Ian S. Zagon, et al.	**Art Unit:**	1635
Serial No.:	09/431,843	**Docket:**	13038
Filed:	November 2, 1999	**Dated:**	April 3, 2000

For: NOVEL NUCLEIC ACID MOLECULES ENCODING OPIOID GROWTH FACTOR RECEPTORS

Assistant Commissioner for Patents
Washington, DC 20231

Response to Notice to Comply under 37 C.F.R.§ 1.821

Sir:

In response to the Office Communication dated February 10, 2000 and in accordance with the provisions in 37 C.F.R. §1.821, Applicants submit herewith a substitute paper and a substitute computer readable copy of the Sequence Listing, along with a Statement Under 37 C.F.R. § 1.821(f), stating that these copies are identical. A copy of the Notice to Comply is also

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CERTIFICATE OF MAILING UNDER 37 C.F.R. § 1.8(a)

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Assistant Commissioner for Patents, Washington, DC 20231 on April 3, 2000.

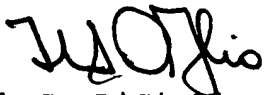
Dated: April 3, 2000

Janet Giordano
Janet Giordano

F:\work\1123\13038\misc\13038.ntc

enclosed. Applicants respectfully submit that the content of the paper and computer copies of the sequence listing does not introduce new matter.

Respectfully submitted,



Frank S. DiGiglio
Registration No. 31,346

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Garden City, New York 11530
(516) 742-4343

FSD/XZ:ab

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

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Assistant Commissioner for Patents
Washington, D.C. 20231

STATEMENT UNDER 37 C.F.R. § 1.821(f)

Sir:

I hereby state that the content of the substitute paper and computer readable copies of the Sequence Listing submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same.

Respectfully submitted,

Frank S. DiGiglio
Registration No. 31,346

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Garden City, New York 11530
(516) 742-4343
FSD/XZ:ab

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Dated: April 3, 2000

Janet Giordano
Janet Giordano

Raw Sequence Listing Error Summary

SERIAL NUMBER: 09/431,843

ERROR DETECTED	SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to :3, as this will prevent "wrapping".

2 ____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 ____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ✓ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 ____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.

8 ____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(I) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
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10 ____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 ____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 ____ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 ____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

SEQUENCE LISTING

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Verderame, Michael
Allen, Sandra
McLaughlin J., Patricia

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                85                  90                  95

Tyr Arg Asn Glu Ile Arg Phe Leu Pro Asn Gly Cys Phe Ile Glu Asp
            100                 105                 110

Ile Leu Gln Asn Trp Thr Asp Asn Tyr Asp Leu Leu Glu Asp Asn His
        115                 120                 125

Ser Tyr Ile Gln Trp Leu Phe Pro Leu Arg Glu Pro Gly Val Asn Trp
    130                 135                 140

His Ala Lys Pro Leu Thr Leu Arg Glu Val Glu Val Phe Lys Ser Ser
145                 150                 155                 160

Gln Glu Ile Gln Glu Arg Leu Val Arg Ala Tyr Glu Leu Met Leu Gly
                165                 170                 175

Phe Tyr Gly Ile Arg Leu Glu Asp Arg Gly Thr Gly Thr Val Gly Arg
            180                 185                 190

Ala Gln Asn Tyr Gln Lys Arg Phe Gln Asn Leu Asn Trp Arg Ser His
        195                 200                 205

Asn Asn Leu Arg Ile Thr Arg Ile Leu Lys Ser Pro Cys Glu Leu Ser
    210                 215                 220

Leu Glu His Phe Gln Ala Pro Leu Val Arg Phe Phe Leu Glu Glu Thr
225                 230                 235                 240

Leu Val Arg Arg Glu Leu Pro Gly Val Arg Gln Ser Ala Leu Asp Tyr
                245                 250                 255

Phe Met Phe Ala Val Arg Cys Arg His Gln Arg Arg Gln Leu Val His
            260                 265                 270

Phe Ala Trp Glu His Phe Arg Pro Arg Cys Lys Phe Val Trp Gly Pro
        275                 280                 285

Gln Asp Lys Leu Arg Arg Phe Lys Pro Ser Ser Leu Pro His Pro Leu
    290                 295                 300

Glu Gly Ser Arg Lys Val Glu Glu Glu Gly Ser Pro Gly Asp Pro Asp
305                 310                 315                 320
```

a' cont

His Glu Ala Ser Thr Gln Gly Arg Thr Cys Glu Pro Glu His Ser Lys
325 330 335

Gly Gly Gly Arg Val Asp Glu Gly Pro Gln Pro Arg Ser Val Glu Pro
340 345 350

Gln Asp Ala Gly Pro Leu Glu Arg Ser Gln Gly Asp Glu Ala Gly Gly
355 360 365

His Gly Glu Asp Arg Pro Glu Pro Leu Ser Pro Lys Glu Ser Lys Lys
370 375 380

Arg Lys Leu Glu Leu Ser Arg Arg Glu Gln Pro Pro Thr Gly Pro Gly
385 390 395 400

Pro Gln Ser Ala Ser Glu Val Glu Lys Ile Ala Leu Asn Leu Glu Gly
405 410 415

Cys Ala Leu Ser Gln Gly Ser Leu Arg Thr Gly Thr Gln Glu Val Gly
420 425 430

Gly Gln Asp Pro Gly Glu Ala Val Gln Pro Cys Arg Gln Pro Leu Gly
435 440 445

Ala Arg Val Ala Asp Lys Val Arg Lys Arg Arg Lys Val Asp Glu Gly
450 455 460

Thr Gly Asp Ser Ala Ala Val Ala Ser Gly Gly Ala Gln Thr Leu Ala
465 470 475 480

Leu Ala Gly Ser Pro Ala Pro Ser Gly His Pro Lys Ala Gly His Ser
485 490 495

Glu Asn Gly Val Glu Glu Asp Thr Glu Gly Arg Thr Gly Pro Lys Glu
500 505 510

Gly Thr Pro Gly Ser Pro Ser Glu Thr Pro Gly Pro Ser Pro Ala Gly
515 520 525

a' cont.

Pro Ala Gly Asp Glu Pro Ala Lys Thr Pro Ser Glu Thr Pro Gly Pro
530 535 540

Ser Pro Ala Gly Pro Thr Arg Asp Glu Pro Ala Glu Ser Pro Ser Glu
545 550 555 560

Thr Pro Gly Pro Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu
565 570 575

Ser Pro Ser Glu Thr Pro Gly Pro Arg Pro Ala Gly Pro Ala Gly Asp
580 585 590

Glu Pro Ala Lys Ile Pro Ser Glu Thr Pro Gly Pro Ser Pro Ala Gly
595 600 605

Pro Thr Arg Asp Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro
610 615 620

```
Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu
625                 630                 635                 640

Thr Pro Gly Pro Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu
                645                 650                 655

Ser Pro Ser Glu Thr Pro Gly Pro Ser Pro Ala Gly Pro Thr Arg Asp
            660                 665                 670

Glu Pro Ala Lys Ala Gly Glu Ala Ala Glu Leu Gln Asp Ala Glu Val
        675                 680                 685

Glu Ser Ser Ala Lys Ser Gly Lys Pro
    690                 695
```

<210> 7
<211> 1601
<212> DNA
<213> Homo sapiens

<400> 7
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gccgccggcg cgagggacgc ggacgcaggg gacgaggacg aggagtcgga ggagccgcgg 180

gcggcgcggc ccagctcgtt ccagtccaga atgacagggt ccagaaactg gcgagccacg 240

agggacatgt gtaggtatcg gcacaactat ccggatctgg tggaacgaga ctgcaatggg 300

gacacgccaa acctgagttt ctacagaaat gagatccgct tcctgcccaa cggctgtttc 360

attgaggaca ttcttcagaa ctggacggac aactatgacc tccttgagga caatcactcc 420

tacatccagt ggctgtttcc tctgcgagaa ccaggagtga actggcatgc caagcccctc 480

acgctcaggg aggtcgaggt gtttaaaagc tcccaggaga tccaggagcg gcttgtccgg 540

gcctacgagc tcatgctggg cttctacggg atccggctgg aggaccgagg cacgggcacg 600

gtgggccgag cacagaacta ccagaagcgc ttccagaacc tgaactggcg cagccacaac 660

aacctccgca tcacacgcat cctcaagtcg ccgtgtgagc tgagcctcga gcacttccag 720

gcgccactgg tccgcttctt cctggaggag acgctggtgc ggcgggagct gccgggggtg 780

cggcagagtg ccctggacta cttcatgttc gccgtgcgct gccgacacca gcgccgccag 840

ctggtgcact tcgcctggga gcacttccgg ccccgctgca agttcgtctg ggggccccaa 900

gacaagctgc ggaggttcaa gcccagctct ctgccgcatc cgctcgaggg ctccaggaag 960

gtggaggagg aaggaagccc cggggacccc gaccacgagg ccagcaccca gggtcggacc 1020

tgtgggccag agcatagcaa gggtgggggc agggtggacg aggggcccca gccacggagc 1080

gtggagcccc aggatgcggg acccctggag aggagccagg gggatgaggc aggggccac 1140

ggggaagata ggccggagcc cttaagcccc aaagagagca agaagaggaa gctggagctg 1200

agccggcggg agcagccgcc cacagagcca ggccctcaga gtgcctcaga ggtggagaag 1260

atcgctctga atttggaggg gtgtgccctc agccagggca gcctcaggac ggggacccag 1320

gaagtgggcg gtcaggaccc tggggaggcc tcctgtccct gctgcagggg ctggggcctc 1380

cggagctgct gcgggctccc ctcaggctct gcttcgtgac ccgtgaccca tgacccacag 1440

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cccaaggcct gcaggagcct cctggcctgg ctgtgtcttc cccacccagc tctcccctgc 1560

gcccctgtct ttgtaaattg acccttctgg agtgggggggc g 1601

<210> 8
<211> 461
<212> PRT
<213> Homo sapiens

<400> 8

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Met Asp Asp Pro Asp Cys Asp Ser Thr Trp Glu Glu Asp Glu Glu Asp
  1               5                  10                  15

Ala Glu Asp Ala Glu Asp Glu Asp Cys Glu Asp Gly Glu Ala Ala Gly
            20                  25                  30

Ala Arg Asp Ala Asp Ala Gly Asp Glu Asp Glu Glu Ser Glu Glu Pro
        35                  40                  45

Arg Ala Ala Arg Pro Ser Ser Phe Gln Ser Arg Met Leu Thr Gly Ser
    50                  55                  60

Arg Asn Trp Arg Ala Thr Arg Asp Met Cys Arg Tyr Arg His Asn Tyr
65                  70                  75                  80

Pro Asp Leu Val Glu Arg Asp Cys Asn Gly Asp Thr Pro Asn Leu Ser
                85                  90                  95

Phe Tyr Arg Asn Glu Ile Arg Phe Leu Pro Asn Gly Cys Phe Ile Glu
            100                 105                 110

Asp Ile Leu Gln Asn Trp Thr Asp Asn Tyr Asp Leu Leu Glu Asp Asn
        115                 120                 125

His Ser Tyr Ile Gln Trp Leu Phe Pro Leu Arg Glu Pro Gly Val Asn
    130                 135                 140
```

a cont.

Trp His Ala Lys Pro Leu Thr Leu Arg Glu Val Glu Val Phe Lys Ser
145 150 155 160

Ser Gln Glu Ile Gln Glu Arg Leu Val Arg Ala Tyr Glu Leu Met Leu
165 170 175

Gly Phe Tyr Gly Ile Arg Leu Glu Asp Arg Gly Thr Gly Thr Val Gly
180 185 190

Arg Ala Gln Asn Tyr Gln Lys Arg Phe Gln Asn Leu Asn Trp Arg Ser
195 200 205

His Asn Asn Leu Arg Ile Thr Arg Ile Leu Lys Ser Pro Cys Glu Leu
210 215 220

Ser Leu Glu His Phe Gln Ala Pro Leu Val Arg Phe Phe Leu Glu Glu
225 230 235 240

Thr Leu Val Arg Arg Glu Leu Pro Gly Val Arg Gln Ser Ala Leu Asp
245 250 255

Tyr Phe Met Phe Ala Val Arg Cys Arg His Gln Arg Arg Gln Leu Val
260 265 270

His Phe Ala Trp Glu His Phe Arg Pro Arg Cys Lys Phe Val Trp Gly
275 280 285

Pro Gln Asp Lys Leu Arg Arg Phe Lys Pro Ser Ser Leu Pro His Pro
290 295 300

Leu Glu Gly Ser Arg Lys Val Glu Glu Glu Gly Ser Pro Gly Asp Pro
305 310 315 320

Asp His Glu Ala Ser Thr Gln Gly Arg Thr Cys Gly Pro Glu His Ser
325 330 335

Lys Gly Gly Gly Arg Val Asp Glu Gly Pro Gln Pro Arg Ser Val Glu
340 345 350

Pro Gln Asp Ala Gly Pro Leu Glu Arg Ser Gln Gly Asp Glu Ala Gly
355 360 365

Gly His Gly Glu Asp Arg Pro Glu Pro Leu Ser Pro Lys Glu Ser Lys
370 375 380

Lys Arg Lys Leu Glu Leu Ser Arg Arg Glu Gln Pro Pro Thr Glu Pro
385 390 395 400

Gly Pro Gln Ser Ala Ser Glu Val Glu Lys Ile Ala Leu Asn Leu Glu
405 410 415

Gly Cys Ala Leu Ser Gln Gly Ser Leu Arg Thr Gly Thr Gln Glu Val
420 425 430

Gly Gly Gln Asp Pro Gly Glu Ala Ser Cys Pro Cys Cys Arg Gly Trp
435 440 445

a' cont.

Gly Leu Arg Ser Cys Cys Gly Leu Pro Ser Gly Ser Ala Ser
450 455 460

<210> 9
<211> 2348
<212> DNA
<213> Homo sapiens

<400> 9
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tgggaggagg acgaggagga tgcggaggac gcggaggacg aggactgcga ggacggcgag 120

gccgccggcg cgagggacgc ggacgcaggg gacgaggacg aggagtcgga ggagccgcgg 180

gcggcgcggc ccagctcgtt ccagtccaga atgacagggt ccagaaactg gcgagccacg 240

agggacatgt gtaggtatcg gcacaactat ccggatctgg tggaacgaga ctgcaatggg 300

gacacgccaa acctgagttt ctacagaaat gagatccgct tcctgcccaa cggctgtttc 360

attgaggaca ttcttcagaa ctggacggac aactatgacc tccttgagga caatcactcc 420

tacatccagt ggctgtttcc tctgcgagaa ccaggagtga actggcatgc caagcccctc 480

acgctcaggg aggtcgaggt gtttaaaagc tcccaggaga tccaggagcg gcttgtccgg 540

gcctacgagc tcatgctggg cttctacggg atccggctgg aggaccgagg cacgggcacg 600

gtgggccgag cacagaacta ccagaagcgc ttccagaacc tgaactggcg cagccacaac 660

aacctccgca tcacacgcat cctcaagtcg ccgtgtgagc tgagcctcga gcacttccag 720

gcgccactgg tccgcttctt cctggaggag acgctggtgc ggcgggagct gccgggggtg 780

cggcagagtg ccctggacta cttcatgttc gccgtgcgct gccgacacca gcgccgccag 840

ctggtgcact tcgcctggga gcacttccgg ccccgctgca agttcgtctg ggggccccaa 900

gacaagctgc ggaggttcaa gcccagctct ctgccgcatc cgctcgaggg ctccaggaag 960

gtggaggagg aaggaagccc cggggacccc gaccacgagg ccagcaccca gggtcggacc 1020

tgtgggccag agcatagcaa gggtgggggc agggtggacg aggggcccca gccacggagc 1080

gtggagcccc aggatgcggg acccctggag aggagccagg gggatgaggc agggggccac 1140

ggggaagata ggccggagcc cttaagcccc aaagagagca agaagaggaa gctggagctg 1200

agccggcggg agcagccgcc cacagagcca ggccctcaga gtgcctcaga ggtggagaag 1260

atcgctctga atttggaggg gtgtgccctc agccagggca gcctcaggac ggggacccag 1320

gaagtgggcg gtcaggaccc tggggaggca gtgcagccct gccgccaacc cctgggagcc 1380

a1 cont

agggtggccg acaaggtgag gaagcggagg aaggtggatg agggtgctgg ggacagtgct 1440

gcggtggcca gtggtggtgc ccagaccttg gcccttgccg ggtcccctgc cccatcgggg 1500

caccccaagg ctggacacag tgagaacggg gttgaggagg acacagaagg tcgaacgggg 1560

cccaaagaag gtacccctgg gagcccatcg gagaccccag gccccagccc agcaggacct 1620

gcaggggacg agccagccga gagcccatcg gagaccccag gcccccgccc agcaggacct 1680

gcaggggacg agccagccga gagcccatcg gagaccccag gcctccgccc ggcaggacct 1740

gcaggggacg agccagccga gaccccatcg gagaccccag gccccagccc ggcaggacct 1800

acaagggatg agccagccga gagcccatcg gagaccccag gcccccgccc ggcaggacct 1860

gcaggggacg agccagccga gagcccatcg gagaccccag gcccccgccc ggcaggacct 1920

gcaggggacg aaccagccga gagcccatcg gagaccccag gccccagccc ggcaggacct 1980

acaagggatg agccagccaa ggcgggggag gcagcagagt tgcaggacgc agaggtggag 2040

tcttctgcca agtctgggaa gccttaagga aaggagtgcc cgtcggcgtc ttggtcctcc 2100

tgtccctgct gcaggggctg gggcctccgg agctgctgcg gactcccctc aggctctgct 2160

tcgtgacccg tgacccatga cccacagtgc tggcctcctg tggggccact atagcagcca 2220

ccagaagccg cgaggccctc agggaagccc aaggcctgca gaagcctcct ggcctggctg 2280

tgtcttcccc acccagctct cccctgcgcc cctgtctttg taaattgacc cttctggagt 2340

gggggggcg 2348

<210> 10
<211> 677
<212> PRT
<213> Homo sapiens

<400> 10

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Met Asp Asp Pro Asp Cys Asp Ser Thr Trp Glu Glu Asp Glu Glu Asp
  1               5                  10                  15

Ala Glu Asp Ala Glu Asp Glu Asp Cys Glu Asp Gly Glu Ala Ala Gly
             20                  25                  30

Ala Arg Asp Ala Asp Ala Gly Asp Glu Asp Glu Glu Ser Glu Glu Pro
         35                  40                  45

Arg Ala Ala Arg Pro Ser Ser Phe Gln Ser Arg Met Thr Gly Ser Arg
     50                  55                  60

Asn Trp Arg Ala Thr Arg Asp Met Cys Arg Tyr Arg His Asn Tyr Pro
 65                  70                  75                  80
```

Asp Leu Val Glu Arg Asp Cys Asn Gly Asp Thr Pro Asn Leu Ser Phe
85 90 95

Tyr Arg Asn Glu Ile Arg Phe Leu Pro Asn Gly Cys Phe Ile Glu Asp
100 105 110

Ile Leu Gln Asn Trp Thr Asp Asn Tyr Asp Leu Leu Glu Asp Asn His
115 120 125

Ser Tyr Ile Gln Trp Leu Phe Pro Leu Arg Glu Pro Gly Val Asn Trp
130 135 140

His Ala Lys Pro Leu Thr Leu Arg Glu Val Glu Val Phe Lys Ser Ser
145 150 155 160

Gln Glu Ile Gln Glu Arg Leu Val Arg Ala Tyr Glu Leu Met Leu Gly
165 170 175

Phe Tyr Gly Ile Arg Leu Glu Asp Arg Gly Thr Gly Thr Val Gly Arg
180 185 190

Ala Gln Asn Tyr Gln Lys Arg Phe Gln Asn Leu Asn Trp Arg Ser His
195 200 205

Asn Asn Leu Arg Ile Thr Arg Ile Leu Lys Ser Pro Cys Glu Leu Ser
210 215 220

Leu Glu His Phe Gln Ala Pro Leu Val Arg Phe Phe Leu Glu Glu Thr
225 230 235 240

Leu Val Arg Arg Glu Leu Pro Gly Val Arg Gln Ser Ala Leu Asp Tyr
245 250 255

Phe Met Phe Ala Val Arg Cys Arg His Gln Arg Arg Gln Leu Val His
260 265 270

Phe Ala Trp Glu His Phe Arg Pro Arg Cys Lys Phe Val Trp Gly Pro
275 280 285

Gln Asp Lys Leu Arg Arg Phe Lys Pro Ser Ser Leu Pro His Pro Leu
290 295 300

Glu Gly Ser Arg Lys Val Glu Glu Glu Gly Ser Pro Gly Asp Pro Asp
305 310 315 320

His Glu Ala Ser Thr Gln Gly Arg Thr Cys Gly Pro Glu His Ser Lys
325 330 335

Gly Gly Gly Arg Val Asp Glu Gly Pro Gln Pro Arg Ser Val Glu Pro
340 345 350

Gln Asp Ala Gly Pro Leu Glu Arg Ser Gln Gly Asp Glu Ala Gly Gly
355 360 365

His Gly Glu Asp Arg Pro Glu Pro Leu Ser Pro Lys Glu Ser Lys Lys
370 375 380

a' cont.

Arg Lys Leu Glu Leu Ser Arg Arg Glu Gln Pro Pro Thr Glu Pro Gly
385 390 395 400

Pro Gln Ser Ala Ser Glu Val Glu Lys Ile Ala Leu Asn Leu Glu Gly
405 410 415

Cys Ala Leu Ser Gln Gly Ser Leu Arg Thr Gly Thr Gln Glu Val Gly
420 425 430

Gly Gln Asp Pro Gly Glu Ala Val Gln Pro Cys Arg Gln Pro Leu Gly
435 440 445

Ala Arg Val Ala Asp Lys Val Arg Lys Arg Arg Lys Val Asp Glu Gly
450 455 460

Ala Gly Asp Ser Ala Ala Val Ala Ser Gly Gly Ala Gln Thr Leu Ala
465 470 475 480

Leu Ala Gly Ser Pro Ala Pro Ser Gly His Pro Lys Ala Gly His Ser
485 490 495

Glu Asn Gly Val Glu Glu Asp Thr Glu Gly Arg Thr Gly Pro Lys Glu
500 505 510

Gly Thr Pro Gly Ser Pro Ser Glu Thr Pro Gly Pro Ser Pro Ala Gly
515 520 525

Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro
530 535 540

Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu
545 550 555 560

Thr Pro Gly Leu Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu
565 570 575

Thr Pro Ser Glu Thr Pro Gly Pro Ser Pro Ala Gly Pro Thr Arg Asp
580 585 590

Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro Arg Pro Ala Gly
595 600 605

Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro
610 615 620

Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu
625 630 635 640

Thr Pro Gly Pro Ser Pro Ala Gly Pro Thr Arg Asp Glu Pro Ala Lys
645 650 655

Ala Gly Glu Ala Ala Glu Leu Gln Asp Ala Glu Val Glu Ser Ser Ala
660 665 670

Lys Ser Gly Lys Pro
675

a' cont.

<210> 11
<211> 2289
<212> DNA
<213> Homo sapiens

<400> 11
tagaattcag cggccgctga attctagccg agcatggacg accccgactg cgactccacc 60

tgggaggagg acgaggagga tgcggaggac gcggaggacg aggactgcga ggacggcgag 120

gccgccggcg cgagggacgc ggacgcaggg gacgaggacg aggagtcgga ggagccgcgg 180

gcggcgcggc ccagctcgtt ccagtccaga atgacagggt ccagaaactg gcgagccacg 240

agggacatgt gtaggtatcg gcacaactat ccggatctgg tggaacgaga ctgcaatggg 300

gacacgccaa acctgagttt ctacagaaat gagatccgct tcctgcccaa cggctgtttc 360

attgaggaca ttcttcagaa ctggacggac aactatgacc tccttgagga caatcactcc 420

tacatccagt ggctgtttcc tctgcgagaa ccaggagtga actggcatgc caagcccctc 480

acgctcaggg aggtcgaggt gtttaaaagc tcccaggaga tccaggagcg gcttgtccgg 540

gcctacgagc tcatgctggg cttctacggg atccggctgg aggaccgagg cacgggcacg 600

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gacaagctgc ggaggttcaa gcccagctct ctgccccatc cgctcgaggg ctccaggaag 960

gtggaggagg aaggaagccc cggggacccc gaccacgagg ccagcaccca gggtcggacc 1020

tgtgggccag agcatagcaa gggtgggggc agggtggacg aggggcccca gccacggagc 1080

gtggagcccc aggatgcggg acccctggag aggagccagg gggatgaggc aggggccac 1140

ggggaagata ggccggagcc cttaagcccc aaagagagca agaagaggaa gctggagctg 1200

agccggcggg agcagccgcc cacagagcca ggccctcaga gtgcctcaga ggtggagaag 1260

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gaagtgggcg gtcaggaccc tggggaggca gtgcagccct gccgccaacc cctgggagcc 1380

agggtggccg acaaggtgag gaagcggagg aaggtggatg agggtgctgg ggacagtgct 1440

gcggtggcca gtggtggtgc ccagaccttg gcccttgccg ggtcccctgc cccatcgggg 1500

caccccaagg ctggacacag tgagaacggg gttgaggagg acacagaagg tcgaacgggg 1560

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acaagggatg agccagccaa ggcgggggag gcagcagagt tgcaggacgc agaggtggag 1980

tcttctgcca agtctgggaa gccttaagga aaggagtgcc cgtcggcgtc ttggtcctcc 2040

tgtccctgct gcaggggctg gggcctccgg agctgctgcg ggctcccctc aggctctgct 2100

tcgtgacccg tgacccatga cccacagtgc tggcctcctg tggggccact atagcagcca 2160

ccagaagccg cgaggccctc agggaagccc aaggcctgca gaagcctcct ggcctggctg 2220

tgtcttcccc acccagctct cccctgcgcc cctgtctttg taaattgacc cttctggagt 2280

gggggggcgg 2289

<210> 12
<211> 657
<212> PRT
<213> Homo sapiens

a1 Cont

<400> 12
Met Asp Asp Pro Asp Cys Asp Ser Thr Trp Glu Glu Asp Glu Glu Asp
1 5 10 15

Ala Glu Asp Ala Glu Asp Glu Asp Cys Glu Asp Gly Glu Ala Ala Gly
20 25 30

Ala Arg Asp Ala Asp Ala Gly Asp Glu Asp Glu Glu Ser Glu Glu Pro
35 40 45

Arg Ala Ala Arg Pro Ser Ser Phe Gln Ser Arg Met Thr Gly Ser Arg
50 55 60

Asn Trp Arg Ala Thr Arg Asp Met Cys Arg Tyr Arg His Asn Tyr Pro
65 70 75 80

Asp Leu Val Glu Arg Asp Cys Asn Gly Asp Thr Pro Asn Leu Ser Phe
85 90 95

Tyr Arg Asn Glu Ile Arg Phe Leu Pro Asn Gly Cys Phe Ile Glu Asp
100 105 110

Ile Leu Gln Asn Trp Thr Asp Asn Tyr Asp Leu Leu Glu Asp Asn His
115 120 125

Ser Tyr Ile Gln Trp Leu Phe Pro Leu Arg Glu Pro Gly Val Asn Trp
130 135 140

His Ala Lys Pro Leu Thr Leu Arg Glu Val Glu Val Phe Lys Ser Ser
145 150 155 160

Gln Glu Ile Gln Glu Arg Leu Val Arg Ala Tyr Glu Leu Met Leu Gly
165 170 175

Phe Tyr Gly Ile Arg Leu Glu Asp Arg Gly Thr Gly Thr Val Gly Arg
180 185 190

Ala Gln Asn Tyr Gln Lys Arg Phe Gln Asn Leu Asn Trp Arg Ser His
195 200 205

Asn Asn Leu Arg Ile Thr Arg Ile Leu Lys Ser Pro Cys Glu Leu Ser
210 215 220

Leu Glu His Phe Gln Ala Pro Leu Val Arg Phe Phe Leu Glu Glu Thr
225 230 235 240

Leu Val Arg Arg Glu Leu Pro Gly Val Arg Gln Ser Ala Leu Asp Tyr
245 250 255

Phe Met Phe Ala Val Arg Cys Arg His Gln Arg Arg Gln Leu Val His
260 265 270

Phe Ala Trp Glu His Phe Arg Pro Arg Cys Lys Phe Val Trp Gly Pro
275 280 285

Gln Asp Lys Leu Arg Arg Phe Lys Pro Ser Ser Leu Pro His Pro Leu
290 295 300

Glu Gly Ser Arg Lys Val Glu Glu Glu Gly Ser Pro Gly Asp Pro Asp
305 310 315 320

His Glu Ala Ser Thr Gln Gly Arg Thr Cys Gly Pro Glu His Ser Lys
325 330 335

Gly Gly Gly Arg Val Asp Glu Gly Pro Gln Pro Arg Ser Val Glu Pro
340 345 350

Gln Asp Ala Gly Pro Leu Glu Arg Ser Gln Gly Asp Glu Ala Gly Gly
355 360 365

His Gly Glu Asp Arg Pro Glu Pro Leu Ser Pro Lys Glu Ser Lys Lys
370 375 380

Arg Lys Leu Glu Leu Ser Arg Arg Glu Gln Pro Pro Thr Glu Pro Gly
385 390 395 400

a1 cont.

Pro Gln Ser Ala Ser Glu Val Glu Lys Ile Ala Leu Asn Leu Glu Gly
405 410 415

Cys Ala Leu Ser Gln Gly Ser Leu Arg Thr Gly Thr Gln Glu Val Gly
420 425 430

Gly Gln Asp Pro Gly Glu Ala Val Gln Pro Cys Arg Gln Pro Leu Gly
435 440 445

Ala Arg Val Ala Asp Lys Val Arg Lys Arg Arg Lys Val Asp Glu Gly
450 455 460

Ala Gly Asp Ser Ala Ala Val Ala Ser Gly Gly Ala Gln Thr Leu Ala
465 470 475 480

Leu Ala Gly Ser Pro Ala Pro Ser Gly His Pro Lys Ala Gly His Ser
485 490 495

Glu Asn Gly Val Glu Glu Asp Thr Glu Gly Arg Thr Gly Pro Lys Glu
500 505 510

Gly Thr Pro Gly Ser Pro Ser Glu Thr Pro Gly Pro Ser Pro Ala Gly
515 520 525

Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro
530 535 540

Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu
545 550 555 560

Thr Pro Gly Pro Ser Pro Ala Gly Pro Thr Arg Asp Glu Pro Ala Glu
565 570 575

Ser Pro Ser Glu Thr Pro Gly Pro Arg Pro Ala Gly Pro Ala Gly Asp
580 585 590

Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro Arg Pro Ala Gly
595 600 605

Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro
610 615 620

Ser Pro Ala Gly Pro Thr Arg Asp Glu Pro Ala Lys Ala Gly Glu Ala
625 630 635 640

Ala Glu Leu Gln Asp Ala Glu Val Glu Ser Ser Ala Lys Ser Gly Lys
645 650 655

Pro

<210> 13
<211> 1232
<212> DNA
<213> Homo sapiens

<400> 13
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ctgggaggag gacgaggagg atgcggagga cgcggaggac gaggactgcg aggacggcga 120

ggccgccggc gcgagggacg cggacgcagg ggacgaggac gaggagtcgg aggagccgcg 180

ggcggcgcgg cccagctcgt tccagtccag aatgacaggg tccagaaact ggcgagccac 240

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Ala Arg Asp Ala Asp Ala Gly Asp Glu Asp Glu Glu Ser Glu Glu Pro
35 40 45

Arg Ala Ala Arg Pro Ser Ser Phe Gln Ser Arg Met Thr Gly Ser Arg
50 55 60

Asn Trp Arg Ala Thr Arg Asp Met Cys Arg Tyr Arg His Asn Tyr Pro
65 70 75 80

Asp Leu Val Glu Arg Asp Cys Asn Gly Asp Thr Pro Asn Leu Ser Phe
85 90 95

Tyr Arg Asn Glu Ile Arg Phe Leu Pro Asn Gly Cys Phe Ile Glu Asp
100 105 110

Ile Leu Gln Asn Trp Thr Asp Asn Tyr Asp Leu Leu Glu Asp Asn His
115 120 125

Ser Tyr Ile Gln Trp Leu Phe Pro Leu Arg Glu Pro Gly Val Asn Trp
130 135 140

His Ala Lys Pro Leu Thr Leu Arg Glu Val Glu Val Phe Lys Ser Ser
145 150 155 160

Gln Glu Ile Gln Glu Arg Leu Val Arg Ala Tyr Glu Leu Met Leu Gly
165 170 175

Phe Tyr Gly Ile Arg Leu Glu Asp Arg Gly Thr Gly Thr Val Gly Arg
180 185 190

Ala Gln Asn Tyr Gln Lys Arg Phe Gln Asn Leu Asn Trp Arg Ser His
195 200 205

Asn Asn Leu Arg Ile Thr Arg Ile Leu Lys Ser Pro Cys Glu Leu Ser
210 215 220

Leu Glu His Phe Gln Ala Pro Leu Val Arg Phe Phe Leu Glu Glu Thr
225 230 235 240

Leu Val Arg Arg Glu Leu Pro Gly Val Arg Gln Ser Ala Leu Asp Tyr
245 250 255

Phe Met Phe Ala Val Arg Cys Arg His Gln Arg Arg Gln Leu Val His
260 265 270

Phe Ala Trp Glu His Phe Arg Pro Arg Cys Lys Phe Val Trp Gly Pro
275 280 285

Gln Asp Lys Leu Arg Arg Phe Lys Pro Ser Ser Leu Pro His Pro Leu
290 295 300

Glu Gly Ser Arg Lys Val Glu Glu Glu Gly Pro Ala Gly Asp Glu Pro
305 310 315 320

Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro Ser Pro Ala Gly Pro Thr
325 330 335

Arg Asp Glu Pro Ala Lys Ala Gly Glu Ala Glu Ala Cys Cys Leu Ala
340 345 350

Val Ser Ser His Pro Ala Leu Pro Cys Ala Pro Val Phe Val Asn Arg
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Pro Phe Trp Ser Gly Gly Arg Arg Ala Gly Leu Ala Phe Leu Ser Leu
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Met Pro Ser Lys Ala Phe Ser Glu
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a' Cont

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